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                                                                                                                                           AL Submitted (08-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries; humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Sep 12, 1999 this sequence version replaced gi:5734384.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00741 Length: 112424bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 112424)
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Submitted (27-NOV-1996) Biochemistry, University of Missouri, 117
Schweitzer Hall, Columbia, MO 65211, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL033383.24 GI:5870348
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KVMNAQKAGASAVLVADDIEEDFLIFMOTPEEDWSSAXTIBATI PSALLGKSRGEKLK
DAIGGGDWINVLUMPERAVHENDIBEETWSKAXTIBATI PSALLGKSRGEKLK
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NCEDIDBCKDKKAQQCPECSCKNIWGSYNCSCSGDLLYIKDODTCISKTASQAKSTWA
AFWYVLIALAMLAGGGTLYYXYRIKQYMDSEIRAIMAQYMFLDSQEGFNHYNHQRG"
55 a 306 c 518 g 552 t
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/db_xref="taxon:9606"
/chromosome="6"
                                                                                                Location/Qualifiers
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/db_xref="taxon:3888"
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Search completed: September 20, 2000, 08:24:58 Job time: 21038 sec

V_segment

join(18598. .18649,18821. .>19113)

gene	mRNA	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region		misc_recomb		misc_recomb		misc_recomb					CDS	9 4	q p p p	V_segment			mRNA	repeat_region	repeat_region	repeat_region		misc_recomb	-	misc_recomb		misc_recomb		
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JOURNAL MEDLINE REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS	JOURNAL MEDI, INE	TITLE	REFERENCE	•	ONGOINTON	SOURCE	VERSION VERSION	DEFINITION	PSU79958		Db 16981	Qy 2:	Matches		repea	repeat	repeat	repeat		misc_:		misc_z		misc_		V_segn						CDS

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2 (bases 1 to 1931)
Paris,N., Rogers,S.W., Jiang,L., Kirsch,T., Beevers,L.,
Phillips,T.E. and Rogers,J.C.
Molecular coloning and further characterization of a probable plant
vacuolar sorting receptor
Plant Physiol. 115 (1), 29-39 (1997)
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Kirsch,T., Paris,N., Butler,J.M., Beevers,J. and Rogers,J.C.
Purification and initial characterization of a potential plant
vacuolar targeting receptor
Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3403-3407 (1994)
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/rpt_family="MIR2"
complement(37473..37661)
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/rpt_family="MIR2"
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Paris, N., Rogers, S.W. and Rogers, J.C

(bases 1 to 1931)

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exon

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intron

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number.

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intron

5194.

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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Meoptera; Endopterygota; Diptera; Brachycera;
pterygota; Neoptera; Endopterygota; Drosophila.
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                              Rockville, MD, USA
Rockville, MD, USA
This sequence was identified as CDM:10211864 by the submitter.
This sequence was identified as CDM:10211864 by the fixed are come.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be preserved.

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* the accession/Qualifiers
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HMRVHGNNNSSNGSNGATGVGGESSTGSGVGGGNSLLT"
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pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
RS Endoptera; Endoptera; Chawez, C., Chew, M., Clasiolka, L.,
RS Entenhoff, C., Champe, M., Chavez, C., Chew, M., Clasiolka, N. L.,
Doyle, C.M., Farifan, D.E., Galle, R., George, R., Harris, N. L.,
Boyle, C.M., Farifan, D.E., A., Hummasti, S.R., Karra, K., Kearney, L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
Kim, E., Lewis, S., Li, P., Lomotan, M.A., Mazda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb J.M., Park, S.,
Moshrefi, A.R., Moshrefi, M., Weinburg, T., Zhang, R., Zieran, L.L. and
Syirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L.
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submitted (22-JUN-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

For further information about this sequence, Including its location

on sep 3, 1999 this sequences, Please visit our sequence

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archive Web site (http://www.fruitfly.org/sequence/) or send email

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LULU/890 LZ1256 bp DNA

HTG BACR02G21 (D722) RPCI-91

Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-91

Drosophila melanogaster chromosome 3 clone BACR02G2 IN PROGRESS

Drosophila melanogaster chromosome 3 clone BACR02G2 IN PROGRESS
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                                                 1059: gap of unknown length
1059: gap of unknown length
1580: contig of 521 bp in length
1660: gap of unknown length
2367: contig of 707 bp in length
2447: gap of unknown length
3319: contig of 872 bp in length
3319: gap of unknown length
4062: contig of 663 bp in length
4142: gap of unknown length
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5113: contig of 663 bp in length
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ORIGIN BASE COUNT

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2226 c

2220 g

2651 t

exon

7981. .9021 /gene="gl"__

/db_xref="FlyBase:FBgn0004618"

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'gene="ql" 'number= 'gene≖"gi

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Query Match Best Local Similarity

Matches

18;

Conservative

90.0%;

Score 16.8; pred. No. 42.

DB 33; 2;

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7129 CCTGGGCTTAAGTCTATCCG 7148

1 cttgggcttacgtctatccg 20

RESULT

AC014473/c

REFERENCE AUTHORS TITLE JOURNAL

Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,

Adams, M. and Venter, J.C. pirect submission

BASE COUNT

22813 a

).rganism-"Drosophila melanogaster" /Organism-"taxon:7227" /db_xref="taxon:7227" /17895 c 18046 g 23147 t

ware Malch

94.0%;

Score 16.8; DB 42; Length 81901; prod. No. 41;

FEATURES

source

SOURCE ORGANISM

KEYWORDS

HTG; HTGS_PHASE2 AC014473.1 GI:6436862

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NA HTG 16-NOV-195

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Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
                                       glass gene, transcription factor; zinc finger protein fruit fly.
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Gunn,T.M., Miller,K.A., He,L., Hyman,R.W., Davis,R.W., Azarani,A., Schlossman,S.F., Duke-Cohan,J.S. and Barsh,G.S.
The mouse mahogany locus encodes a transmembrane form of human
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Gunn, T.M., Miller, K.A., He, L., Hyman, R.W., Davis, R.W., Azarani, A., Direct Submission
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6879, 6957
/gene="mg"
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/db_xref="taxon:10090"
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          The open reading frame in the cDNA segs, derived from a different wild-type strain differs at four positions from that of the genomic
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The glass gene encodes a zinc-finger protein required by Drosophila
photoreceptor cells
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Submitted (19-JUL-1989) Moses K., Howard Hughes Medical Institute,
Department of Biochemistry, University of California, Room 539 LSA,
Berkeley California 94720
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                                                                                                                                                                     /product="glass protein"
/protein_id="cAA33450.1"
/db_xref="GI:8016"
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/clone="5F2"
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/db_xref="taxon:7227"
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RESULT 2 PARRN2SS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Query Matches Best Local Matches Qy 1 1 GA	RESULT 1 A98413 LOCUS DEFINITION ACCESSION VERSION KEYNORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE ORGANISM REFERENCE AUTHORS TOURNAL FEATURES SOURCE ORIGIN	4444444 5540000000000000000000000000000
PARRN23S 2893 bp DNA Pseudomonas aeruginosa gene for 23S ribo Y00432.1 GI:45420 23S ribosomal RNA; ribosomal DNA. Pseudomonas aeruginosa. Pseudomonas aeruginosa Bacteria; Proteobacteria; gamma subdivis Pseudomonas. 1 (bases 1 to 2893) Ulbrich, N. Direct Submission	h 100.0%; score 20; DB 5; Similarity 100.0%; Pred. No. 6.8; 20; Conservative 0; Mismatches 0; Laggottggtgttaagc 20	A98413 20 bp DNA Sequence 2 from Patent WO9912949. A98413.1 GI:6781514 . unidentified. unidentified unidentified. (bases 1 to 20) 1 (bases 1 to 20) 1 (bases 1 to 20) 2 rype GENUS PSEUDOMONAS PATENT: WO 9912949-A 18-MAR-1999; ROLFS ARNDT (DE); BRAEUER ANJA (DE) Location/Qualifiers 1. 20 /organism="unidentified" /db_xref="taxon:32644" 4 a 2 c 9 9	18.4 92.0 2905 2 AF053963 18.4 92.0 2906 2 SEU77927 18.4 92.0 2906 2 SEU77921 18.4 92.0 2906 2 SEU77923 18.4 92.0 2906 2 SEU77923 18.4 92.0 2906 2 SEU77924 18.4 92.0 2907 5 E16366 18.4 92.0 2907 5 E16366 18.4 92.0 2908 2 SEU77920 18.4 92.0 2908 2 SEU77920 18.4 92.0 2908 2 SEU77926 18.4 92.0 2975 1 SA23SSGA1 18.4 92.0 3029 1 CSPLSURR 18.4 92.0 3029 1 CSPLSURR 18.4 92.0 5203 2 TCU78300 18.4 92.0 5679 2 AF134704 18.4 92.0 5679 1 AB035923 18.4 92.0 6561 1 AB035923 18.4 92.0 6811 1 AB035924
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2 (Dases 1 to 2893)
7 (Dases 1, Hopfl, P., Ludwig, W., Schleifer, K.H., Ulbrich, N. and Toschka, H.Y., Hopfl, P., Ludwig, W., Schleifer, K.H., Ulbrich, N.
                                                                                                                                                                                                                                                                                                              Christensen,H.
Direct Submission
Direct Submission
Submitted (12-NOV-1996) Veterinary Microbiology, Royal Veterinary and Agricultural University, Bulowsvej 13, Frederiksberg 1870,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia enterocolitica.
Yersinia enterocolitica
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Complete nucleotide sequence of a 23S ribosomal RNA gene from Pseudomonas aeruginosa
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Christensen, H., Nordentoft, S. and Olsen, J.E.
Christensen, H., Nordentoft, S. and Olsen, J.E.
Phylogenetic relationships of Salmonella based on rRNA sequences
Int. J. Syst. Bacteriol. 48 Pt 2, 605-610 (1998)
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/strain="ATCC 10145"
/db_xref="taxon:287"
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/$train="NCTC10460 (jeo2341)"
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